

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:37 ; Search time 170.72 Seconds
(without alignments)
27.443 Million cell updates/sec

Title: US-09-331-631A-5_COPY_76_144
Perfect score: 381
Sequence: 1 NRQRDPQQQYEQCQKRCQRR.....EEQREDEKYEERKMEGDN 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 1008

Database :

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	173	45.4	566	2	S22477	vicilin precursor
2	147.5	38.7	509	2	S08059	alpha-globulin typ
3	145.5	38.2	588	1	FMCMAB	alpha-globulin a p
4	128	33.6	605	2	S06398	alpha-globulin tYP
5	115	30.2	810	2	T44430	protein pVI100 (imp
6	114.5	30.1	1038	2	T02634	rep protein homoid
7	105.5	27.7	385	2	T19201	hypothetical prote
8	103	27.0	1898	1	A43573	trichovallin - hum
9	102	26.8	6173	2	S27770	trichovallin - hyp
10	101	26.5	1737	2	A59335	hypothetical prote
11	100	26.2	1407	1	S28589	unconventional myo
12	99	26.0	1390	2	T14004	trichovallin - rab
13	97.5	25.6	839	2	S0590	trifla protein - sll
14	97.5	25.6	1077	2	I50591	Class I INCENP pro
15	97.5	25.6	827	2	T46481	Class II INCENP pr
16	97.5	25.6	1233	2	T30989	hypothetical protea
17	95.5	25.1	483	2	T06459	serine/threonine p
18	95.5	25.1	1023	2	S12519	62k sucrose-bindin
19	95	24.9	524	2	J01730	glutacitin - fruit
20	95	24.7	905	1	RG8YS5	62k sucrose-bindin
21	94	24.7	233	2	T17218	regulatory protein
22	94	24.7	648	1	J01150	hypothetical prote
23	94	24.7	1085	2	S62516	protein kinase (EC
24	93.5	24.5	781	2	T02272	hypothetical coile
25	93	24.4	139	2	A26892	hypothetical prote
26	93	24.4	429	2	S29565	Mopa box protein -
27	93	24.4	523	2	T24961	apolipoprotein A-I
28	93	24.4	849	2	S61962	hypothetical prote
29	92.5	24.3	1403	2	S24548	probable membrane
						homoeotic protein p

30	91.5	24.0	406	2	T24492	hypothetical prote
31	91.5	24.0	540	2	S21825	vicillin-like stora
32	91.5	24.0	573	2	A53234	globin-15, GLB15
33	91	23.9	385	2	T20410	hypothetical prote
34	90	23.6	678	2	A54514	glutamic acid-rich
35	90	23.6	1344	2	T42637	hypothetical prote
36	89.5	23.5	758	2	S54522	hypothetical prote
37	89	23.4	285	1	I46207	involucrin - dog
38	89	23.4	582	2	B53234	vicilin-like stora
39	88.5	23.2	407	2	T03258	globulin - maize
40	88	23.1	292	2	JE0233	tropomyosin-I - scall
41	88	23.1	447	2	S52391	centroscomin B - mo
42	88	23.1	766	2	G54024	protein kinase (EC
43	88	23.1	778	2	H54024	protein kinase (EC
44	88	23.1	767	2	F54024	protein kinase (EC
45	88	23.1	779	2	E54024	protein kinase (EC

ALIGNMENTS

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RESULT      1
S22477
vicillin precursor - cacao
C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478# S18105; S22050
R:McHenry, L.; Fritzt, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A>Title: Comparison of the structure and nucleotide sequence of vicillin genes of cacao
A:Reference number: S22477; MUID:92288309
A:Accession: S22477
A:Molecule type: DNA
A:Residues: 1-566 <MCH>
A:Cross-references: EMBL:X62625
A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626
C:Genetics:
A:introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-566/Product: vicillin #status predicted <MAT>

Query Match          45.4%   Score 173; DB 2; Length 566;
Best Local Similarity 32.6%; Pred.No. 1.5e-07;
Matches    31; Conservative 17; Mismatches 15; Indels 32; Gaps 1;

OY       3 QRDPOQDYECCKRCORRETERPRHMQICQRCCRRYEKKRKQQ-----46
            ::::|||||::: | | | : ||||| ::::|:|:
DB       35 ERDPQQEYECORRCESEATEREEDEOCERCEYKFKQROBEELDROYQQCGRCQE 94
            ::::|||||::: | | | : ||||| ::::|:|:
OY       47 -----KRVEQOREDEEKYEERNK 65
            :::||:|:|:| | | | | |
DB       95 QQGCGREDQCCKRCWEQYKEGRGEHENYRNHKK 129

RESULT      2
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N:Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A>Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S08398
A:Accession: S08059
A>Status: not compared with conceptual translation

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submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23035
A:Accession: T46481
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1027 <AAAs>
A:Cross-references: EMBL:AL137755
A:Experimental source: adult testis; clone DKFZp434A025
C:Genetics:
A:Note: DKFZp434A025.1

Query Match 25.6%; Score 97.5; DB 2; Length 1027;
Best Local Similarity 39.2%; Pred. No. 0.43;
Matches 29; Conservative 17; Mismatches 17; Indels 11; Gaps 4;

OY 2 RQDPDOOYECCOK--RCQRETEPRHMQIOQRCERRYEKKRK---QOKRYEEOOR- 54
DB 134 RQKRIEQQKQRRRLQEQQRREARQOQREOR--RRQEEKRRLLELERRRKEEEERR 191
OY 55 --EDDEKYEERRKE 66
DB 192 RAEEKKRRVEREQE 205

Search completed: March 1, 2001, 15:52:38
Job time: 562 sec

